

SEQUENCE LISTING

<110> Fox, Brian
Holloway, James L.

<120> ADIPOCYTE COMPLMENT RELATED PROTEIN
ZACRP13

<130> 00-96

<150> US 60/253,924

<151> 2000-11-29

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<221> CDS

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Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	Gly	Glu	Ile	Ser	Glu	Met	
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Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe	
85 90 95	
gct tgc agg gtg cct ggg aat tac tac tcc agc ttt gat gtt gag ctg	337
Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu	
100 105 110	
cat cat tgc aag gtg aat att tgg cta atg agg aag caa att ttg gct	385
His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala	
115 120 125	
aat aag gaa gaa att tct aag cag caa agc att caa gag gtg act tgg	433
Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp	
130 135 140	
gtg ctg tta aag gca ttc agt ttc ata agg gag gca gag cat aag agt	481
Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser	
145 150 155 160	
tca gaa aat ttg cac cct gac aat gtg ata aaa aag aaa aac cca ttt	529
Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe	
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Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu	
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Lys	Gly	Asn	Val	Gly	Trp	Glu	Pro	Pro	His	Arg	Val	Pro	Ser	Gly	Ala	
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Pro	Ser	Ser	Arg	Ala	Val	Arg	Arg	Ser	Pro	Pro	Ser	Ser	Arg	Leu	Gln	
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Asp	Thr	Gln	Cys	Gln	Pro	Val	Lys	Ala	Ala	Gly	Met	Glu	Ser	Val	Pro	
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 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr
 195 200 205
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro
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 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val
 225 230 235 240
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala
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 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu
 260 265 270
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile
 275 280 285
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe
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 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln
 305 310 315 320
 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
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 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
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 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
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 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
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 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
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 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
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of SEQ ID NO:2

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<223> Each n is independently A, T, G, or C.

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<223> n = A.T.C or G

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ttyacngtna	arytnwsngg	naarytnccn	ytnccnttya	arccnathat	httyacnggn	240
gtnyntaya	aygcncarmg	ngayytnaar	gargcnatgg	gngtnttygc	ntgymngtn	300
ccnggnaayt	aytaywsnws	nttygaygt	garytncayc	aytgyaargt	naayathtg	360
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gargtnacnt	gggtnytnyt	naargcntty	wsnttyathm	gngargcnga	rcayaarwsn	480
wsngaraaay	tncayccnga	yaaygttnath	aaraaraara	ayccnttyws	ngarggnaar	540
ttyaarytng	cngcngarat	htgyathtgy	aaygargary	tnaaygtnaa	yccncargay	600
aayggngara	ayathwsntg	gacntgycar	mgnwsnwsnc	arcarwsnat	haarwsnytn	660
gcntggmgnc	cnmgnmgnaa	rtggttytgy	ggnacnggnc	cnggnwsnyt	ntgytgygt	720
carccnmng	ayytngtncc	ntgygtncn	gtnaaywsng	cngtngcnws	ngarggngcn	780
wsnccnaarc	cntggcaryt	nccnwsnggn	gtngarccng	tnggngcnaa	raarwsnmgn	840
athgargtn	gggarccnc	nathmgntty	caraarath	ayggnaaycc	ntggatgccn	900
mgncaraart	tygcngtngg	ngtnggnwsn	wsntggmgna	cnwsngcnmg	ngtngtncar	960
aarggnaayg	tnggntggga	rcncncncay	mgngtnccnw	snggngcncc	nwsnwsnmgn	1020
gcngtnmgm	gnwsnccnc	nwsnwsnmgn	ytncaraarg	gnmgnwsnac	ngaywsnytn	1080
carcaygtnc	cngaraarws	nacngayacn	cartgycarc	cngtnaargc	ngcnggnatg	1140
garwsngtn	cntayaarac	ngtngtngcn	garytnacna	aracngtngg	nathtayytn	1200
ytncaytgyc	aygayytnga	ygtngmgncay	ggngtnaarm	gngaycaytt	yggngcnnytn	1260
mgnttygayt	gyccnacngg	nttymgnaen	tayatgggnc	cngtnccnyt	ntgyttygg	1320
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<213> Artificial Sequence

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<223> Aromatic motif

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<223> Each Xaa is any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

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<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan, or leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

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<222> (26)...(26)

<223> Xaa is any amino acid residue

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<222> (28)...(31)

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Lys	Cys	Cys	Ile	Gly	Glu	Met	Gly	Tyr	Met	Arg	Val	Thr	Met	Gly	Arg	
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Ala	Gly	Asp	Thr	Glu	Val	Lys	Lys	Thr	Gly	Phe	Leu	Gln	Glu	Leu	Thr	
			50					55					60			

ttc	cag	cag	gag	cct	ggc	atc	tcc	tcc	tct	cct	tct	tgc	tcc	cgc	tct	240
Phe	Gln	Gln	Glu	Pro	Gly	Ile	Ser	Ser	Ser	Pro	Ser	Cys	Ser	Arg	Ser	
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tgc	cat	gtg	aca	cca	cct	gct	cca	cct	gca	tct	tct	gcc	ata	att	gta	288
Cys	His	Val	Thr	Pro	Pro	Ala	Pro	Pro	Ala	Ser	Ser	Ala	Ile	Ile	Val	
							85				90				95	

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Arg	Phe	Leu	Arg	Pro	Ser	Pro	Glu	Ala	Asp	Ala	Ser	Ser	Met	Leu	Ile	
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Ala	Gln	Ser	Val	Glu	Pro	Ile	Val	Val	Ile	Pro	Val	Leu	Ile	Thr	Ala	
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gtc	att	gag	cat	gta	gaa	gtt	gct	gga	cct	cca	gca	cac	ccc	agg	ccc	432
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Ser	Ala	Phe	Thr	Val	Lys	Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys		
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Pro	Ile	Ile	Phe	Thr	Gly	Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys		
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Glu	Ala	Met	Gly	Val	Phe	Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser		
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Ser	Phe	Asp	Val	Glu	Leu	His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met		
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Ile	Gln	Glu	Val	Thr	Trp	Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg		
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Glu	Ala	Glu	His	Lys	Ser	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile		
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Lys	Lys	Lys	Asn	Pro	Phe	Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu		
	290					295					300						

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gaa aat atc tcc tgg aca tgt cag agg tct tca cag cag tcc atc aaa Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys 325 330 335	1008
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ggg tcc ctg tgc tgt gtg cag cct aga gac ttg gtg ccc tgt gtc cca Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro 355 360 365	1104
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ctt cca agt ggt gtt gag cct gtg ggt gca aag aag tca aga att gag Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu 385 390 395 400	1200
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tct gca agg gta gta caa aag gga aat gtt ggg tgg gag ccc cca cac Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His 435 440 445	1344
aga gtc ccc agt ggg gct cca tct agt aga gct gtg aga aga agt cca Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro 450 455 460	1392
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<213> Homo sapiens
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Phe	Gln	Gln	Glu	Pro	Gly	Ile	Ser	Ser	Ser	Pro	Ser	Cys	Ser	Arg	Ser
65					70					75					80
Cys	His	Val	Thr	Pro	Pro	Ala	Pro	Pro	Ala	Ser	Ser	Ala	Ile	Ile	Val
				85					90					95	
Arg	Phe	Leu	Arg	Pro	Ser	Pro	Glu	Ala	Asp	Ala	Ser	Ser	Met	Leu	Ile
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Ala	Gln	Ser	Val	Glu	Pro	Ile	Val	Val	Ile	Pro	Val	Leu	Ile	Thr	Ala
		115					120					125			
Val	Ile	Glu	His	Val	Glu	Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro
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145					150					155					160
Gly	Glu	Ile	Ser	Glu	Met	Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg
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Pro	Ile	Ile	Phe	Thr	Gly	Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys
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Glu	Ala	Met	Gly	Val	Phe	Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser
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225					230					235					240
Arg	Lys	Gln	Ile	Leu	Ala	Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser
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			260					265					270		
Glu	Ala	Glu	His	Lys	Ser	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile
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Glu	Asn	Ile	Ser	Trp	Thr	Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys
				325					330					335	
Ser	Leu	Ala	Trp	Arg	Pro	Arg	Arg	Lys	Trp	Phe	Cys	Gly	Thr	Gly	Pro
			340					345					350		
Gly	Ser	Leu	Cys	Cys	Val	Gln	Pro	Arg	Asp	Leu	Val	Pro	Cys	Val	Pro
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Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln
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 Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu
 385 390 395 400
 Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp
 405 410 415
 Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr
 420 425 430
 Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His
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 Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His
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 Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala
 485 490 495
 Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys
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 Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His
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 Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr
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<211> 1731

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<220>

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of SEQ ID NO:6

<221> misc_feature

<222> (1)...(1731)

<223> n = A,T,C or G

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cargarytna	cnttycarca	rgarccnggn	athwsnwsnw	sncnwsntg	ywsnmgnwsn	240
tgycaygtna	cncncncng	nccncncng	wsnwsngcna	thathgtngm	nttyytnmgn	300
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